

1  
SEQUENCE LISTING

<110> Shaaltiel, Yoseph  
Baum, Gideon  
Sharon Hashmueli  
Ayala Lewkowicz  
Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<160> 14

<170> PatentIn version 3.3

<210> 1  
<211> 22  
<212> PRT  
<213> Artificial sequence

<220>  
<223> ER signal peptide

<400> 1

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala Glu Phe  
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<210> 2  
<211> 7  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Vacuolar targeting signal from Tobacco chitinase A

<400> 2

Asp Leu Leu Val Asp Thr Met  
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<210> 3  
<211> 21  
<212> DNA  
<213> Artificial sequence

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<223> Single strand DNA oligonucleotide

<400> 3  
cagaattcgc ccgccctgc a 21

<210> 4  
<211> 22  
<212> DNA  
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<220>  
<223> Single strand DNA oligonucleotide

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ctcagatctt ggcatgcca ca 22

<210> 5  
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<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 5

ctcagaagac cagaggct

19

<210> 6

<211> 17

<212> DNA

<213> Artificial sequence

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caaagcggcc atcgtgc

17

<210> 7

<211> 1491

<212> DNA

<213> Homo sapiens

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gagagtacac gcagtgggag acggatggag ctgagtatgg ggcccatcca ggctaatacac 180

acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga 240

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caaaatttgc tacttaaata gtacttctct gaagaaggaa tcggatataa catcatccgg 360

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gctgagcaca agttacagtt ctgggcagtg acagctgaaa atgagccttc tgctgggctg 720

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gccgtgacc taggtcctac cctcgccaac agtactcacc acaatgtccg cctactcatg 840

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<210> 8  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 8

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 1 5 10 15

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 20 25 30

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg  
 35 40 45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly  
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly  
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu  
 85 90 95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu  
 100 105 110

Gly Val Arg Leu Leu Met Leu Asn Asp Gln Arg Leu Leu Leu Pro His  
 115 120 125

Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His  
 130 135 140

Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys Ala  
 145 150 155 160

Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe Ala  
 165 170 175

Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg Leu  
 180 185 190

Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn  
 195 200 205

Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn  
 210 215 220

Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile  
 225 230 235 240

Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr

245	250	255
His Leu Gly	His Phe Ser Lys Phe Ile Pro Glu Gly Ser	Gln Arg Val
260	265	270
Gly Leu Val	Ala Ser Gln Lys Asn Asp Leu Asp Ala Val	Ala Leu Met
275	280	285
His Pro Asp Gly Ser Ala Val	Val Val Val Leu Asn Arg Ser Ser Lys	
290	295	300
Asp Val Pro Leu Thr	Ile Lys Asp Pro Ala Val Gly Phe Leu Glu Thr	
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Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln		
325	330	335

<210> 9  
 <211> 338  
 <212> DNA  
 <213> Cauliflower mosaic virus  
  
 <400> 9  
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 ggaaaggcta tcgttcaaga tgctctacc gacagtggc ccaaagatgg acccccaccc 180  
 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240  
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 tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10  
 <211> 66  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Nucleic acid sequence encoding the ER signal peptide  
  
 <400> 10  
 atgaagacta atctttttct ctttctcatc ttttcacttc tcctatcatt atcctcgcc 60  
 gaattc 66

<210> 11  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Nucleic acid sequence encoding the vacuolar targeting sequence  
  
 <400> 11  
 gatcttttag tcgatactat g 21

<210> 12  
 <211> 167  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

<220>  
 <221> misc\_feature  
 <222> (162)..(162)  
 <223> n is a, c, g, or t

<400> 12  
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 agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120  
 ttataataa acaaagactt tgtcccaaaa accccccccc cngcaga 167

<210> 13  
 <211> 2186  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> nucleic acid sequence encoding high mannose human  
 glucocerebrosidase (GCD)

<220>  
 <221> misc\_feature  
 <222> (2181)..(2181)  
 <223> n is a, c, g, or t

<400> 13  
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 ggaaaggcta tcgttcaaga tgctctacc gacagtggtc ccaaagatgg acccccaccc 180  
 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240  
 tgtgatattc cactgacgt aagggatgac gcacaatccc actatccttc gcaagacctt 300  
 tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac 360  
 aattaccaac aacaacaaac aacaaacaac attacaatta ctatttaca ttacagtcga 420  
 gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt 480  
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 gaacagaagt tccagaaagt gaagggattt ggaggggcca tgacagatgc tgctgctctc 780  
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 tgtattccct tgcaatgcag ggcctagggc tatgaataaa gttaatgtgt gaatgtgtga 2100  
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<210> 14  
 <211> 526  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> High mannose human glucocerebrosidase (GCD)

<400> 14

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
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Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly  
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Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe  
 35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser  
 50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala  
 65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys  
 85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala  
 100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Lys  
 115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro  
 130 135 140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr  
 145 150 155 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr  
 165 170 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg  
 180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
 195 200 205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly  
 210 215 220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp  
 225 230 235 240

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn  
 245 250 255

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly  
 260 265 270

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro  
 275 280 285

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp  
 290 295 300

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp  
 305 310 315 320

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
 325 330 335

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu  
 340 345 350

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys  
 355 360 365

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln  
 370 375 380

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp  
 385 390 395 400

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val  
 405 410 415

Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr  
 420 425 430

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe  
 435 440 445

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn  
 450 455 460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val  
 465 470 475 480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp  
 485 490 495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His  
 500 505 510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met  
 515 520 525